Sequence Listing

<110> Botstein,David
Desnoyers,Luc
Ferrara,Napoleone
Fong,Sherman
Gao,Wei-Qiang
Goddard,Audrey
Gurney,Austin L.
Pan,James
Roy,Margaret Ann
Stewart,Timothy A.
Tumas,Daniel
Watanabe,Colin K.
Wood,William I.

<120> Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

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35 40 45

Phe Ala Ile Ala Arg Arg Leu Ala Gln Asp Gly Ala His Val Val
50 55 60

Val Ser Ser Arg Lys Gln Gln Asn Val Asp Gln Ala Val Ala Thr
65 70 75

Leu Gln Gly Glu Gly Leu Ser Val Thr Gly Thr Val Cys His Val
80 85 90

Gly Lys Ala Glu Asp Arg Glu Arg Leu Val Ala Thr Ala Val Lys
95 100 105

Leu His Gly Gly Ile Asp Ile Leu Val Ser Asn Ala Ala Val Asn
110 115 120

Pro Phe Phe Gly Ser Ile Met Asp Val Thr Glu Glu Val Trp Asp
125 130 135

Lys Thr Leu Asp Ile Asn Val Lys Ala Pro Ala Leu Met Thr Lys
140 145 150

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155 160 165

Ile Val Ser Ser Ile Ala Ala Phe Ser Pro Ser Pro Gly Phe Ser
170 175 180

Pro Tyr Asn Val Ser Lys Thr Ala Leu Leu Gly Leu Thr Lys Thr
185 190 195

Leu Ala Ile Glu Leu Ala Pro Arg Asn Ile Arg Val Asn Cys Leu
200 205 210

Ala Pro Gly Leu Ile Lys Thr Ser Phe Ser Arg Met Leu Trp Met
215 220 225

Asp Lys Glu Lys Glu Glu Ser Met Lys Glu Thr Leu Arg Ile Arg
230 235 240

Arg Leu Gly Glu Pro Glu Asp Cys Ala Gly Ile Val Ser Phe Leu
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Gly	Trp	Gly	Gly	Leu	Arg	Leu	Leu	Asn	Gly	Leu	Pro	Pro	Gly	Ser
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Phe	Val	Pro	Arg	Pro	His	Thr	Ala	Pro	Leu	Gly	Gly	Ala	His	Ala
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His	Val	Leu	Gly	Met	Val	Pro	Pro	Ala	Cys	Leu	Pro	Gly	Asp	Glu
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Val	Gly	Ser	Glu	Gln	Arg	Gly	Glu	Gln	Val	Thr	Asn	Gly	Arg	Glu
				80				85					90	

Ala	Gly	Ala	Glu	Leu	Leu	Thr	Glu	Val	Asn	Arg	Leu	Gly	Ser	Gly
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Arg Arg Thr Leu His Leu Arg Arg Asn Arg Ile Ser Asn Cys Ser
125 130 135

Gln Arg Ala Gly Ala Arg Pro Gly Ser Leu Pro Glu Arg Lys Gly
140 145 150

Pro Glu Leu Cys Leu Glu Glu Leu Asp Ala Ala Ile Pro Gly Ser
155 160 165

Arg Ala Val Gly Gly Ser Lys Ala Arg Val Gln Ala Arg Gln Val
170 175 180

Pro Pro Ala Thr Ala Ser Glu Trp Arg Leu Ala Gln Ala Gln Gln
185 190 195

Lys Ile Arg Glu Leu Ala Ile Asn Ile Arg Met Lys Glu Glu Leu
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Ile Gly Glu Leu Val Arg Thr Gly Lys Ala Ala Gln Ala Leu Asn
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230 235 240

Gln Val Arg Ala Glu Leu Ser Glu Gly Gln Arg Gln Leu Arg Glu
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Leu Glu Gly Lys Glu Leu Gln Asp Ala Gly Glu Arg Ser Arg Leu
260 265 270

Gln Glu Phe Arg Arg Arg Val Ala Ala Ala Gln Ser Gln Val Gln
275 280 285

Val Leu Lys Glu Lys Lys Gln Ala Thr Glu Arg Leu Val Ser Leu
290 295 300

Ser Ala Gln Ser Glu Lys Arg Leu Gln Glu Leu Glu Arg Asn Val
305 310 315

Gln Leu Met Arg Gln Gln Gln Gly Gln Leu Gln Arg Arg Leu Arg
320 325 330

Glu Glu Thr Glu Gln Lys Arg Arg Leu Glu Ala Glu Met Ser Lys
335 340 345

Arg Gln His Arg Val Lys Glu Leu Glu Leu Lys His Glu Gln Gln
350 355 360

Gln Lys Ile Leu Lys Ile Lys Thr Glu Glu Ile Ala Ala Phe Gln
365 370 375

Arg Lys Arg Arg Ser Gly Ser Asn Gly Ser Val Val Ser Leu Glu
380 385 390

Gln Gln Gln Lys Ile Glu Glu Gln Lys Lys Trp Leu Asp Gln Glu

395 400 405

Met Glu Lys Val Leu Gln Gln Arg Arg Ala Leu Glu Glu Leu Gly
410 415 420

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425 430 435

Leu Met Gln Glu Lys Thr Gly Leu Glu Ser Lys Arg Leu Arg Ser
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Ser Gln Ala Leu Asn Glu Asp Ile Val Arg Val Ser Ser Arg Leu
455 460 465

Glu His Leu Glu Lys Glu Leu Ser Glu Lys Ser Gly Gln Leu Arg
470 475 480

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Leu Leu Cys Lys Tyr Phe Asp Lys Val Val Thr Leu Arg Glu Glu
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Arg Ile Gln Ala Leu Glu Lys Glu Leu Gly Arg Tyr Met Trp Ile
680 685 690

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695 700 705

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710 715 720

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725 730 735

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740 745 750

Glu Thr Arg Asp Leu Val His Ala Pro Leu Pro Leu Thr Trp Lys
755 760 765

Arg Ser Ser Leu Cys Gly Glu Glu Gln Gly Ser Pro Glu Glu Leu
770 775 780

Arg Gln Arg Glu Ala Ala Glu Pro Leu Val Gly Arg Val Leu Pro
785 790 795

Val Gly Glu Ala Gly Leu Pro Trp Asn Phe Gly Pro Leu Ser Lys
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Pro Arg Arg Glu Leu Arg Arg Ala Ser Pro Gly Met Ile Asp Val
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Arg Lys Asn Pro Leu
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35 40 45

Lys Ile Tyr Asn Pro Ser Glu Gln Cys Cys Tyr Asp Asp Ala Ile
50 55 60

Leu Ser Leu Lys Glu Thr Arg Arg Cys Gly Ser Thr Cys Thr Phe
65 70 75

Trp Pro Cys Phe Glu Leu Cys Cys Pro Glu Ser Phe Gly Pro Gln
80 85 90

Gln Lys Phe Leu Val Lys Leu Arg Val Leu Gly Met Lys Ser Gln
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Cys His Leu Ser Pro Ile Ser Arg Ser Cys Thr Arg Asn Arg Arg
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His Val Leu Tyr Pro
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Glu	Leu	Gly	Arg	Pro	Ala	Arg	Asp	Glu	Gly	Gly	Ser	Gly	Arg	Asp	
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Trp	Lys	Ser	Lys	Ser	Gly	Arg	Gly	Leu	Ala	Gly	Arg	Glu	Pro	Trp	
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Ser	Lys	Leu	Lys	Gln	Ala	Trp	Val	Ser	Gln	Gly	Gly	Gly	Ala	Lys	
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Ala	Gly	Asp	Leu	Gln	Val	Arg	Pro	Arg	Gly	Asp	Thr	Pro	Gln	Ala	
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Glu	Ala	Leu	Ala	Ala	Ala	Ala	Gln	Asp	Ala	Ile	Gly	Pro	Glu	Leu	
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Ala	Pro	Thr	Pro	Glu	Pro	Pro	Glu	Glu	Tyr	Val	Tyr	Pro	Asp	Tyr	
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Arg	Gly	Lys	Gly	Cys	Val	Asp	Glu	Ser	Gly	Phe	Val	Tyr	Ala	Ile	
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Gly	Glu	Lys	Phe	Ala	Pro	Gly	Pro	Ser	Ala	Cys	Pro	Cys	Leu	Cys	
				170					175						180
Thr	Glu	Glu	Gly	Pro	Leu	Cys	Ala	Gln	Pro	Glu	Cys	Pro	Arg	Leu	
				185					190						195
His	Pro	Arg	Cys	Ile	His	Val	Asp	Thr	Ser	Gln	Cys	Cys	Pro	Gln	
				200					205						210
Cys	Lys	Glu	Arg	Lys	Asn	Tyr	Cys	Glu	Phe	Arg	Gly	Lys	Thr	Tyr	
				215					220						225

Gln Thr Leu Glu Glu Phe Val Val Ser Pro Cys Glu Arg Cys Arg

230 235 240

Cys Glu Ala Asn Gly Glu Val Leu Cys Thr Val Ser Ala Cys Pro
245 250 255

Gln Thr Glu Cys Val Asp Pro Val Tyr Glu Pro Asp Gln Cys Cys
260 265 270

Pro Ile Cys Lys Asn Gly Pro Asn Cys Phe Ala Glu Thr Ala Val
275 280 285

Ile Pro Ala Gly Arg Glu Val Lys Thr Asp Glu Cys Thr Ile Cys
290 295 300

His Cys Thr Tyr Glu Glu Gly Thr Trp Arg Ile Glu Arg Gln Ala
305 310 315

Met Cys Thr Arg His Glu Cys Arg Gln Met
320 325

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<400> 13
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<212> DNA
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<400> 15

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gccaaggacc aggagccccg cgtcactgag caccggatgg gccccggcct 300

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<213> Homo sapiens

<400> 16

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His Val Trp Lys Val Ser Asp Leu Pro Arg Gln Trp Thr Pro Lys
             35                  40                  45

Asn Thr Ser Cys Asp Ser Gly Leu Gly Cys Gln Asp Thr Leu Met
             50                  55                  60

Leu Ile Glu Ser Gly Pro Gln Val Ser Leu Val Leu Ser Lys Gly
             65                  70                  75

Cys Thr Glu Ala Lys Asp Gln Glu Pro Arg Val Thr Glu His Arg
             80                  85                  90

Met Gly Pro Gly Leu Ser Leu Ile Ser Tyr Thr Phe Val Cys Arg
             95                 100                 105

Gln Glu Asp Phe Cys Asn Asn Leu Val Asn Ser Leu Pro Leu Trp
            110                 115                 120

Ala Pro Gln Pro Pro Ala Asp Pro Gly Ser Leu Arg Cys Pro Val
            125                 130                 135

Cys Leu Ser Met Glu Gly Cys Leu Glu Gly Thr Thr Glu Glu Ile
            140                 145                 150

Cys Pro Lys Gly Thr Thr His Cys Tyr Asp Gly Leu Leu Arg Leu
            155                 160                 165

Arg Gly Gly Gly Ile Phe Ser Asn Leu Arg Val Gln Gly Cys Met
            170                 175                 180

Pro Gln Pro Gly Cys Asn Leu Leu Asn Gly Thr Gln Glu Ile Gly
            185                 190                 195

Pro Val Gly Met Thr Glu Asn Cys Asn Arg Lys Asp Phe Leu Thr
            200                 205                 210

Cys His Arg Gly Thr Thr Ile Met Thr His Gly Asn Leu Ala Gln
            215                 220                 225

Glu Pro Thr Asp Trp Thr Thr Ser Asn Thr Glu Met Cys Glu Val
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230 235 240

Gly Gln Val Cys Gln Glu Thr Leu Leu Leu Ile Asp Val Gly Leu
245 250 255

Thr Ser Thr Leu Val Gly Thr Lys Gly Cys Ser Thr Val Gly Ala
260 265 270

Gln Asn Ser Gln Lys Thr Thr Ile His Ser Ala Pro Pro Gly Val
275 280 285

Leu Val Ala Ser Tyr Thr His Phe Cys Ser Ser Asp Leu Cys Asn
290 295 300

Ser Ala Ser Ser Ser Ser Val Leu Leu Asn Ser Leu Pro Pro Gln
305 310 315

Ala Ala Pro Val Pro Gly Asp Arg Gln Cys Pro Thr Cys Val Gln
320 325 330

Pro Leu Gly Thr Cys Ser Ser Gly Ser Pro Arg Met Thr Cys Pro
335 340 345

Arg Gly Ala Thr His Cys Tyr Asp Gly Tyr Ile His Leu Ser Gly
350 355 360

Gly Gly Leu Ser Thr Lys Met Ser Ile Gln Gly Cys Val Ala Gln
365 370 375

Pro Ser Ser Phe Leu Leu Asn His Thr Arg Gln Ile Gly Ile Phe
380 385 390

Ser Ala Arg Glu Lys Arg Asp Val Gln Pro Pro Ala Ser Gln His
395 400 405

Glu Gly Gly Gly Ala Glu Gly Leu Glu Ser Leu Thr Trp Gly Val
410 415 420

Gly Leu Ala Leu Ala Pro Ala Leu Trp Trp Gly Val Val Cys Pro
425 430 435

Ser Cys

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<212> DNA
<213> Homo sapiens

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gctccgtggc gggaccctga gctgctggag gggacctgca ccccggtgca 250

gctggtcgcc ctcattcgcc acggcacccg ctaccccacg gtcaaacaga 300

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<211> 487
<212> PRT
<213> Homo sapiens

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Ala Ala Ala Leu Ala Ala Ala Leu Leu Ser Ser Leu Ala Arg Cys
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Ser Leu Leu Glu Pro Arg Asp Pro Val Ala Ser Ser Leu Ser Pro
35 40 45

Tyr Phe Gly Thr Lys Thr Arg Tyr Glu Asp Val Asn Pro Val Leu
50 55 60

Leu Ser Gly Pro Glu Ala Pro Trp Arg Asp Pro Glu Leu Leu Glu
65 70 75

Gly Thr Cys Thr Pro Val Gln Leu Val Ala Leu Ile Arg His Gly
80 85 90

Thr Arg Tyr Pro Thr Val Lys Gln Ile Arg Lys Leu Arg Gln Leu
95 100 105

His Gly Leu Leu Gln Ala Arg Gly Ser Arg Asp Gly Gly Ala Ser

110 115 120

Ser Thr Gly Ser Arg Asp Leu Gly Ala Ala Leu Ala Asp Trp Pro
125 130 135

Leu Trp Tyr Ala Asp Trp Met Asp Gly Gln Leu Val Glu Lys Gly
140 145 150

Arg Gln Asp Met Arg Gln Leu Ala Leu Arg Leu Ala Ser Leu Phe
155 160 165

Pro Ala Leu Phe Ser Arg Glu Asn Tyr Gly Arg Leu Arg Leu Ile
170 175 180

Thr Ser Ser Lys His Arg Cys Met Asp Ser Ser Ala Ala Phe Leu
185 190 195

Gln Gly Leu Trp Gln His Tyr His Pro Gly Leu Pro Pro Pro Asp
200 205 210

Val Ala Asp Met Glu Phe Gly Pro Pro Thr Val Asn Asp Lys Leu
215 220 225

Met Arg Phe Phe Asp His Cys Glu Lys Phe Leu Thr Glu Val Glu
230 235 240

Lys Asn Ala Thr Ala Leu Tyr His Val Glu Ala Phe Lys Thr Gly
245 250 255

Pro Glu Met Gln Asn Ile Leu Lys Lys Val Ala Ala Thr Leu Gln
260 265 270

Val Pro Val Asn Asp Leu Asn Ala Asp Leu Ile Gln Val Ala Phe
275 280 285

Phe Thr Cys Ser Phe Asp Leu Ala Ile Lys Gly Val Lys Ser Pro
290 295 300

Trp Cys Asp Val Phe Asp Ile Asp Asp Ala Lys Val Leu Glu Tyr
305 310 315

Leu Asn Asp Leu Lys Gln Tyr Trp Lys Arg Gly Tyr Gly Tyr Thr
320 325 330

Ile Asn Ser Arg Ser Ser Cys Thr Leu Phe Gln Asp Ile Phe Gln
335 340 345

His Leu Asp Lys Ala Val Glu Gln Lys Gln Arg Ser Gln Pro Ile
350 355 360

Ser Ser Pro Val Ile Leu Gln Phe Gly His Ala Glu Thr Leu Leu
365 370 375

Pro Leu Leu Ser Leu Met Gly Tyr Phe Lys Asp Lys Glu Pro Leu
380 385 390

Thr Ala Tyr Asn Tyr Lys Lys Gln Met His Arg Lys Phe Arg Ser
395 400 405

Gly Leu Ile Val Pro Tyr Ala Ser Asn Leu Ile Phe Val Leu Tyr
410 415 420

His Cys Glu Asn Ala Lys Thr Pro Lys Glu Gln Phe Arg Val Gln
425 430 435

Met Leu Leu Asn Glu Lys Val Leu Pro Leu Ala Tyr Ser Gln Glu
440 445 450

Thr Val Ser Phe Tyr Glu Asp Leu Lys Asn His Tyr Lys Asp Ile
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Asn Ser Thr Ser Asp Glu Leu
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<211> 3554
<212> DNA
<213> Homo sapiens

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ccca 3554

<210> 20
<211> 310
<212> PRT
<213> Homo sapiens

<400> 20

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35 40 45

Phe Glu Ser Val Glu Leu Ser Cys Ile Ile Thr Asp Ser Gln Thr
50 55 60

Ser Asp Pro Arg Ile Glu Trp Lys Lys Ile Gln Asp Glu Gln Thr
65 70 75

Thr Tyr Val Phe Phe Asp Asn Lys Ile Gln Gly Asp Leu Ala Gly
80 85 90

Arg Ala Glu Ile Leu Gly Lys Thr Ser Leu Lys Ile Trp Asn Val
95 100 105

Thr Arg Arg Asp Ser Ala Leu Tyr Arg Cys Glu Val Val Ala Arg
110 115 120

Asn Asp Arg Lys Glu Ile Asp Glu Ile Val Ile Glu Leu Thr Val
125 130 135

Gln Val Lys Pro Val Thr Pro Val Cys Arg Val Pro Lys Ala Val
140 145 150

Pro Val Gly Lys Met Ala Thr Leu His Cys Gln Glu Ser Glu Gly
155 160 165

His Pro Arg Pro His Tyr Ser Trp Tyr Arg Asn Asp Val Pro Leu
170 175 180

Pro Thr Asp Ser Arg Ala Asn Pro Arg Phe Arg Asn Ser Ser Phe
185 190 195

His Leu Asn Ser Glu Thr Gly Thr Leu Val Phe Thr Ala Val His
200 205 210

Lys Asp Asp Ser Gly Gln Tyr Tyr Cys Ile Ala Ser Asn Asp Ala
215 220 225

Gly Ser Ala Arg Cys Glu Glu Gln Glu Met Glu Val Tyr Asp Leu
230 235 240

Asn Ile Gly Gly Ile Ile Gly Gly Val Leu Val Val Leu Ala Val
245 250 255

Leu Ala Leu Ile Thr Leu Gly Ile Cys Cys Ala Tyr Arg Arg Gly
260 265 270

Tyr Phe Ile Asn Asn Lys Gln Asp Gly Glu Ser Tyr Lys Asn Pro
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Gly Lys Pro Asp Gly Val Asn Tyr Ile Arg Thr Asp Glu Glu Gly

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Asp Phe Arg His Lys Ser Ser Phe Val Ile
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gctgcagtgg ctggacagcc ctggcgtgga gggcgggccc ctgcgggcac 1000

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gcggacacca gcgactcccg ggcgttggag aaccgagggg cggatgccag 2150

catggcctgc cggaagctgg cggtggcgca cccgctgctg ctgctcaggc 2200

acctgcccat gatcgcggcg ctcctgcacg gccgcaccca cctcaacttc 2250

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<210> 22
<211> 1029
<212> PRT
<213> Homo sapiens

<400> 22

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Ile Trp Phe Pro Glu Glu Lys Pro Leu Pro Thr Ala Phe Leu Val
35 40 45

Asp Thr Ser Glu Glu Ala Leu Leu Leu Pro Asp Trp Leu Lys Leu
50 55 60

Arg Met Ile Arg Ser Glu Val Leu Arg Leu Val Asp Ala Ala Leu
65 70 75

Gln Asp Leu Glu Pro Gln Gln Leu Leu Leu Phe Val Gln Ser Phe
80 85 90

Gly Ile Pro Val Ser Ser Met Ser Lys Leu Leu Gln Phe Leu Asp
95 100 105

Gln Ala Val Ala His Asp Pro Gln Thr Leu Glu Gln Asn Ile Met
110 115 120

Asp Lys Asn Tyr Met Ala His Leu Val Glu Val Gln His Glu Arg
125 130 135

Gly Ala Ser Gly Gly Gln Thr Phe His Ser Leu Leu Thr Ala Ser
140 145 150

Leu Pro Pro Arg Arg Asp Ser Thr Glu Ala Pro Lys Pro Lys Ser
155 160 165

Ser Pro Glu Gln Pro Ile Gly Gln Gly Arg Ile Arg Val Gly Thr
170 175 180

Gln Leu Arg Val Leu Gly Pro Glu Asp Asp Leu Ala Gly Met Phe
185 190 195

Leu Gln Ile Phe Pro Leu Ser Pro Asp Pro Arg Trp Gln Ser Ser
200 205 210

Ser Pro Arg Pro Val Ala Leu Ala Leu Gln Gln Ala Leu Gly Gln
215 220 225

Glu Leu Ala Arg Val Val Gln Gly Ser Pro Glu Val Pro Gly Ile
230 235 240

Thr Val Arg Val Leu Gln Ala Leu Ala Thr Leu Leu Ser Ser Pro
245 250 255

His Gly Gly Ala Leu Val Met Ser Met His Arg Ser His Phe Leu
260 265 270

Ala Cys Pro Leu Leu Arg Gln Leu Cys Gln Tyr Gln Arg Cys Val
275 280 285

Pro Gln Asp Thr Gly Phe Ser Ser Leu Phe Leu Lys Val Leu Leu
290 295 300

Gln Met Leu Gln Trp Leu Asp Ser Pro Gly Val Glu Gly Gly Pro
305 310 315

Leu Arg Ala Gln Leu Arg Met Leu Ala Ser Gln Ala Ser Ala Gly
320 325 330

Arg Arg Leu Ser Asp Val Arg Gly Gly Leu Leu Arg Leu Ala Glu
335 340 345

Ala Leu Ala Phe Arg Gln Asp Leu Glu Val Val Ser Ser Thr Val
350 355 360

Arg Ala Val Ile Ala Thr Leu Arg Ser Gly Glu Gln Cys Ser Val
365 370 375

Glu Pro Asp Leu Ile Ser Lys Val Leu Gln Gly Leu Ile Glu Val
380 385 390

Arg Ser Pro His Leu Glu Glu Leu Leu Thr Ala Phe Phe Ser Ala

395 400 405

Thr Ala Asp Ala Ala Ser Pro Phe Pro Ala Cys Lys Pro Val Val
410 415 420

Val Val Ser Ser Leu Leu Leu Gln Glu Glu Glu Pro Leu Ala Gly
425 430 435

Gly Lys Pro Gly Ala Asp Gly Gly Ser Leu Glu Ala Val Arg Leu
440 445 450

Gly Pro Ser Ser Gly Leu Leu Val Asp Trp Leu Glu Met Leu Asp
455 460 465

Pro Glu Val Val Ser Ser Cys Pro Asp Leu Gln Leu Arg Leu Leu
470 475 480

Phe Ser Arg Arg Lys Gly Lys Gly Gln Ala Gln Val Pro Ser Phe
485 490 495

Arg Pro Tyr Leu Leu Thr Leu Phe Thr His Gln Ser Ser Trp Pro
500 505 510

Thr Leu His Gln Cys Ile Arg Val Leu Leu Gly Lys Ser Arg Glu
515 520 525

Gln Arg Phe Asp Pro Ser Ala Ser Leu Asp Phe Leu Trp Ala Cys
530 535 540

Ile His Val Pro Arg Ile Trp Gln Gly Arg Asp Gln Arg Thr Pro
545 550 555

Gln Lys Arg Arg Glu Glu Leu Val Leu Arg Val Gln Gly Pro Glu
560 565 570

Leu Ile Ser Leu Val Glu Leu Ile Leu Ala Glu Ala Glu Thr Arg
575 580 585

Ser Gln Asp Gly Asp Thr Ala Ala Cys Ser Leu Ile Gln Ala Arg
590 595 600

Leu Pro Leu Leu Leu Ser Cys Cys Cys Gly Asp Asp Glu Ser Val
605 610 615

Arg Lys Val Thr Glu His Leu Ser Gly Cys Ile Gln Gln Trp Gly
620 625 630

Asp Ser Val Leu Gly Arg Arg Cys Arg Asp Leu Leu Leu Gln Leu
635 640 645

Tyr Leu Gln Arg Pro Glu Leu Arg Val Pro Val Pro Glu Val Leu
650 655 660

Leu His Ser Glu Gly Ala Ala Ser Ser Ser Val Cys Lys Leu Asp
665 670 675

Gly Leu Ile His Arg Phe Ile Thr Leu Leu Ala Asp Thr Ser Asp
680 685 690

Ser Arg Ala Leu Glu Asn Arg Gly Ala Asp Ala Ser Met Ala Cys
695 700 705

Arg Lys Leu Ala Val Ala His Pro Leu Leu Leu Leu Arg His Leu
710 715 720

Pro Met Ile Ala Ala Leu Leu His Gly Arg Thr His Leu Asn Phe
725 730 735

Gln Glu Phe Arg Gln Gln Asn His Leu Ser Cys Phe Leu His Val
740 745 750

Leu Gly Leu Leu Glu Leu Leu Gln Pro His Val Phe Arg Ser Glu
755 760 765

His Gln Gly Ala Leu Trp Asp Cys Leu Leu Ser Phe Ile Arg Leu
770 775 780

Leu Leu Asn Tyr Arg Lys Ser Ser Arg His Leu Ala Ala Phe Ile
785 790 795

Asn Lys Phe Val Gln Phe Ile His Lys Tyr Ile Thr Tyr Asn Ala
800 805 810

Pro Ala Ala Ile Ser Phe Leu Gln Lys His Ala Asp Pro Leu His
815 820 825

Asp Leu Ser Phe Asp Asn Ser Asp Leu Val Met Leu Lys Ser Leu
830 835 840

Leu Ala Gly Leu Ser Leu Pro Ser Arg Asp Asp Arg Thr Asp Arg
845 850 855

Gly Leu Asp Glu Glu Gly Glu Glu Glu Ser Ser Ala Gly Ser Leu
860 865 870

Pro Leu Val Ser Val Ser Leu Phe Thr Pro Leu Thr Ala Ala Glu
875 880 885

Met Ala Pro Tyr Met Lys Arg Leu Ser Arg Gly Gln Thr Val Glu
890 895 900

Asp Leu Leu Glu Val Leu Ser Asp Ile Asp Glu Met Ser Arg Arg
905 910 915

Arg Pro Glu Ile Leu Ser Phe Phe Ser Thr Asn Leu Gln Arg Leu
920 925 930

Met Ser Ser Ala Glu Glu Cys Cys Arg Asn Leu Ala Phe Ser Leu
935 940 945

Ala Leu Arg Ser Met Gln Asn Ser Pro Ser Ile Ala Ala Ala Phe
950 955 960

Leu Pro Thr Phe Met Tyr Cys Leu Gly Ser Gln Asp Phe Glu Val
965 970 975

Val Gln Thr Ala Leu Arg Asn Leu Pro Glu Tyr Ala Leu Leu Cys

980 985 990

Gln Glu His Ala Ala Val Leu Leu His Arg Ala Phe Leu Val Gly
995 1000 1005

Met Tyr Gly Gln Met Asp Pro Ser Ala Gln Ile Ser Glu Ala Leu
1010 1015 1020

Arg Ile Leu His Met Glu Ala Val Met
1025

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<211> 2186
<212> DNA
<213> Homo sapiens

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cgccttcctc tcgctgtcct ggtacgcggc actcagcggc cagaaaggcg 150

acgttgtgga cgtttaccag cgggagttcc tggcgctgcg cgatcggttg 200

cacgcagctg agcaggagag cctcaagcgc tccaaggagc tcaacctggt 250

gctggacgag atcaagaggg ccgtgtcaga aaggcaggcg ctgcgagacg 300

gagacggcaa tcgcacctgg ggccgcctaa cagaggaccc ccgattgaag 350

ccgtggaacg gctcacaccg gcacgtgctg cacctgccca ccgtcttcca 400

tcacctgcca cacctgctgg ccaaggagag cagtctgcag cccgcggtgc 450

gcgtgggcca gggccgcacc ggagtgtcgg tggtgatggg catcccgagc 500

gtgcggcgcg aggtgcactc gtacctgact gacactctgc actcgctcat 550

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ctccccccac ttctaccctg acttctcccg cctccgagag tcctttgggg 750

accccaagga gagagtcagg tggaggacca aacagaacct cgattactgc 800

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ggatgacatc gtggccaagc ccaactacct gagcaccatg aagaactttg 900

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ggcttcattg gtaagatgtt caagtcgctg gacctgagcc tgattgtaga 1000

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atattctgtg ggtgaaagtc tgcaaccccg agaaggatgc gaagcactgt 1100

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attcttggat acatttgatt ttttcacgta agtccacata tacttctata 2100

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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2186

<210> 24
<211> 548
<212> PRT
<213> Homo sapiens

<400> 24

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Leu	Cys	Ala	Phe	Leu	Ser	Leu	Ser	Trp	Tyr	Ala	Ala	Leu	Ser	Gly
				20					25					30

Gln Lys Gly Asp Val Val Asp Val Tyr Gln Arg Glu Phe Leu Ala
35 40 45

Leu Arg Asp Arg Leu His Ala Ala Glu Gln Glu Ser Leu Lys Arg
50 55 60

Ser Lys Glu Leu Asn Leu Val Leu Asp Glu Ile Lys Arg Ala Val
65 70 75

Ser Glu Arg Gln Ala Leu Arg Asp Gly Asp Gly Asn Arg Thr Trp
80 85 90

Gly Arg Leu Thr Glu Asp Pro Arg Leu Lys Pro Trp Asn Gly Ser
95 100 105

His Arg His Val Leu His Leu Pro Thr Val Phe His His Leu Pro
110 115 120

His Leu Leu Ala Lys Glu Ser Ser Leu Gln Pro Ala Val Arg Val
125 130 135

Gly Gln Gly Arg Thr Gly Val Ser Val Val Met Gly Ile Pro Ser
140 145 150

Val Arg Arg Glu Val His Ser Tyr Leu Thr Asp Thr Leu His Ser
155 160 165

Leu Ile Ser Glu Leu Ser Pro Gln Glu Lys Glu Asp Ser Val Ile
170 175 180

Val Val Leu Ile Ala Glu Thr Asp Ser Gln Tyr Thr Ser Ala Val
185 190 195

Thr Glu Asn Ile Lys Ala Leu Phe Pro Thr Glu Ile His Ser Gly
200 205 210

Leu Leu Glu Val Ile Ser Pro Ser Pro His Phe Tyr Pro Asp Phe
215 220 225

Ser Arg Leu Arg Glu Ser Phe Gly Asp Pro Lys Glu Arg Val Arg
230 235 240

Trp Arg Thr Lys Gln Asn Leu Asp Tyr Cys Phe Leu Met Met Tyr
245 250 255

Ala Gln Ser Lys Gly Ile Tyr Tyr Val Gln Leu Glu Asp Asp Ile
260 265 270

Val Ala Lys Pro Asn Tyr Leu Ser Thr Met Lys Asn Phe Ala Leu
275 280 285

Gln Gln Pro Ser Glu Asp Trp Met Ile Leu Glu Phe Ser Gln Leu
290 295 300

Gly Phe Ile Gly Lys Met Phe Lys Ser Leu Asp Leu Ser Leu Ile
305 310 315

Val Glu Phe Ile Leu Met Phe Tyr Arg Asp Lys Pro Ile Asp Trp

320 325 330

Leu Leu Asp His Ile Leu Trp Val Lys Val Cys Asn Pro Glu Lys
335 340 345

Asp Ala Lys His Cys Asp Arg Gln Lys Ala Asn Leu Arg Ile Arg
350 355 360

Phe Lys Pro Ser Leu Phe Gln His Val Gly Thr His Ser Ser Leu
365 370 375

Ala Gly Lys Ile Gln Lys Leu Lys Asp Lys Asp Phe Gly Lys Gln
380 385 390

Ala Leu Arg Lys Glu His Val Asn Pro Pro Ala Glu Val Ser Thr
395 400 405

Ser Leu Lys Thr Tyr Gln His Phe Thr Leu Glu Lys Ala Tyr Leu
410 415 420

Arg Glu Asp Phe Phe Trp Ala Phe Thr Pro Ala Ala Gly Asp Phe
425 430 435

Ile Arg Phe Arg Phe Phe Gln Pro Leu Arg Leu Glu Arg Phe Phe
440 445 450

Phe Arg Ser Gly Asn Ile Glu His Pro Glu Asp Lys Leu Phe Asn
455 460 465

Thr Ser Val Glu Val Leu Pro Phe Asp Asn Pro Gln Ser Asp Lys
470 475 480

Glu Ala Leu Gln Glu Gly Arg Thr Ala Thr Leu Arg Tyr Pro Arg
485 490 495

Ser Pro Asp Gly Tyr Leu Gln Ile Gly Ser Phe Tyr Lys Gly Val
500 505 510

Ala Glu Gly Glu Val Asp Pro Ala Phe Gly Pro Leu Glu Ala Leu
515 520 525

Arg Leu Ser Ile Gln Thr Asp Ser Pro Val Trp Val Ile Leu Ser
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Glu Ile Phe Leu Lys Lys Ala Asp
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<210> 25
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

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<210> 26
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<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 26
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<223> Synthetic Oligonucleotide Probe

<400> 27
actcgggatt cctgctgtt 19

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<220>
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<400> 28
aggcctttac ccaaggccac aac 23

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<220>
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<400> 29
ggcctgtcct gtgttctca 19

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<223> Synthetic Oligonucleotide Probe

<400> 30
tcccaccact tacttccatg aa 22

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<212> DNA

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<400> 31
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<210> 32
<211> 23
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<223> Synthetic Oligonucleotide Probe

<400> 32
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 33
gtccagcaag ccctcatt 18

<210> 34
<211> 20
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<223> Synthetic Oligonucleotide Probe

<400> 34
cttctgggcc acagccctgc 20

<210> 35
<211> 21
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<223> Synthetic Oligonucleotide Probe

<400> 35
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<210> 36
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<223> Synthetic Oligonucleotide Probe

<400> 36
ccagtcaggc cgttttaga 19

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<223> Synthetic Oligonucleotide Probe

<400> 37
cgggcgccca agtaaaagct c 21

<210> 38
<211> 28
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 38
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